



PCT10

#10

RAW SEQUENCE LISTING

DATE: 08/06/2002

PATENT APPLICATION: US/10/018,383A

TIME: 16:33:38

Input Set : A:\X11600.ST25.txt

Output Set: N:\CRF3\08062002\J018383A.raw

ENTERED

3 <110> APPLICANT: Becker, Gerald

4 Hale, John

5 Heath, William

6 Johnstone, Edward

7 Little, Sheila

8 Tu, Yuan

9 Yeh, Wu-Kuang

10 Yin, Tinggui

12 <120> TITLE OF INVENTION: Amyloid Precursor Protein Protease and Related Nucleic Acid

Compounds

14 <130> FILE REFERENCE: X-11600

C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/018,383A

C--> 16 <141> CURRENT FILING DATE: 2002-07-08

16 <160> NUMBER OF SEQ ID NOS: 5

18 <170> SOFTWARE: PatentIn version 3.1

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 1683

22 <212> TYPE: DNA

23 <213> ORGANISM: Homo sapiens

25 <220> FEATURE:

26 <221> NAME/KEY: misc_feature

27 <222> LOCATION: (25)..(1629)

28 <223> OTHER INFORMATION: CDS

31 <220> FEATURE:

32 <221> NAME/KEY: misc_feature

33 <222> LOCATION: (1285)..(1365)

34 <223> OTHER INFORMATION: n = any nucleotide A, C, G, or T

37 <400> SEQUENCE: 1

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40 catgtgggtg cagccctggg agcactgtgg ttctgcctca caggagccct ggaggtccag      120
42 gtccctgaag acccagtggg ggcaactgtg ggcaaccgat ccaccctgtg ctgctccttc      180
44 tcccttgagc ctggcttcag cctggcacag ctcaacctca tctggcagct gacagatacc      240
46 aaacagcttg tgcacagctt tgctgagggc caggaccagg gcagcgccta tgccaaccgc      300
48 acggccctct tcccggacct gctggcacag ggcaacgcat ccctgaggct gcagcgcgtg      360
50 cgtgtggcgg acgagggcag cttcacctgc ttctgtagca tccgggattt cggcagcgct      420
52 gccgtcagcc tgcaggtggc cgctccctac tcgaagccca gcatgacctt ggagcccaac      480
54 aaggacctgc ggccagggga cacggtgacc atcacgtgct ccagctacca gggctaccct      540
56 gaggtgagg tggtctggca ggatgggcag ggtgtgcccc tgactggcaa cgtgaccacg      600
58 tcgcagatgg ccaacgagca gggcttgttt gatgtgcaca gcatcctgcg ggtggtgctg      660
60 ggtgcaaatt gcacctacag ctgcctgggt cgcaaccccg tgctgcagca ggatgcgcac      720
62 agctctgtca ccatcacacc ccagagaagc cccacaggag ccgtggagggt ccagggtccct      780
64 gaggaccggt tgggtggccct agtgggcacc gatgccaccc tgcgctgctc cttctccccc      840
66 gagcctgggt tcagcctggc acagctcaac ctcatctggc agctgacaga caccaaaacg      900
68 ctggtgcaca gtttcaccga aggccgggac cagggcagcg cctatgcca cgcacggcc      960

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70 ctcttcccgg acctgctggc acaaggcaat gcatccctga ggctgcagcg cgtgcgtgtg 1020
72 gcgagacgagg gcagcttcac ctgcttcgtg agcatccggg atttcggcag cgctgccgtc 1080
74 agcctgcagg tggccgctcc ctactcgaag cccagcatga ccctggagcc caacaaggac 1140
76 ctgcggccag gggacacggt gaccatcacg tgctccagct accggggcta ccctgaggct 1200
78 gaggtgttct ggcaggatgg gcagggtgtg cccctgactg gcaacgtgac cagctgcag 1260
W--> 80 atggccaacg agcagggtt gtttntnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1320
W--> 82 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnngatgc gcacggctct 1380
84 gtcaccatca cagggcagcc tatgacattc cccccagagg ccctgtgggt gaccgtgggg 1440
86 ctgtctgtct gtctcattgc actgctgggt gccctggctt tcgtgtgctg gagaaagatc 1500
88 aaacagagct gtgaggagga gaatgcagga gctgaggacc aggatgggga gggagaaggc 1560
90 tccaagacag ccctgcagcc tctgaaacac tctgacagca aagaagatga tggacaagaa 1620
92 atagcctgac catgaggacc agggagctgc taccctctcc tacagctct accctctggc 1680
94 tgc 1683
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98 <211> LENGTH: 534
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
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103 <221> NAME/KEY: MISC_FEATURE
104 <222> LOCATION: (421)..(447)
105 <223> OTHER INFORMATION: Xaa at locations 421 through 447 stand for Ala, Cys, Asp,
Glu, Ph
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107 l, Trp, or Tyr
110 <400> SEQUENCE: 2
112 Met Leu Arg Arg Arg Gly Ser Pro Gly Met Gly Val His Val Gly Ala
113 1 5 10 15
116 Ala Leu Gly Ala Leu Trp Phe Cys Leu Thr Gly Ala Leu Glu Val Gln
117 20 25 30
120 Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu
121 35 40 45
124 Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn
125 50 55 60
128 Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala
129 65 70 75 80
132 Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe
133 85 90 95
136 Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val
137 100 105 110
140 Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp
141 115 120 125
144 Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys
145 130 135 140
148 Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr
149 145 150 155 160
152 Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val
153 165 170 175
156 Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr
157 180 185 190
160 Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Ile Leu

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161          195          200          205
164 Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn
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168 Pro Val Leu Gln Gln Asp Ala His Ser Ser Val Thr Ile Thr Pro Gln
169 225          230          235          240
172 Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro Glu Asp Pro Val
173          245          250          255
176 Val Ala Leu Val Gly Thr Asp Ala Thr Leu Arg Cys Ser Phe Ser Pro
177          260          265          270
180 Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr
181          275          280          285
184 Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly Arg Asp Gln Gly
185          290          295          300
188 Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln
189 305          310          315          320
192 Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly
193          325          330          335
196 Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val
197          340          345          350
200 Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu
201          355          360          365
204 Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser
205          370          375          380
208 Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln
209 385          390          395          400
212 Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu
213          405          410          415
W--> 216 Gln Gly Leu Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
217          420          425          430
W--> 220 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp
221          435          440          445
224 Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Met Thr Phe Pro Pro
225          450          455          460
228 Glu Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu
229 465          470          475          480
232 Leu Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys
233          485          490          495
236 Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly
237          500          505          510
240 Ser Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp
241          515          520          525
244 Asp Gly Gln Glu Ile Ala
245          530
248 <210> SEQ ID NO: 3
249 <211> LENGTH: 1683
250 <212> TYPE: DNA
251 <213> ORGANISM: Homo sapiens
253 <220> FEATURE:
254 <221> NAME/KEY: CDS

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255 <222> LOCATION: (25)..(1629)
256 <223> OTHER INFORMATION:
259 <220> FEATURE:
260 <221> NAME/KEY: misc_feature
261 <222> LOCATION: (25)..(1629)
262 <223> OTHER INFORMATION:
265 <400> SEQUENCE: 3
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268                               1                               5
270 atg ggt gtg cat gtg ggt gca gcc ctg gga gca ctg tgg ttc tgc ctc      99
271 Met Gly Val His Val Gly Ala Ala Leu Gly Ala Leu Trp Phe Cys Leu
272 10                               15                               20                               25
274 aca gga gcc ctg gag gtc cag gtc cct gaa gac cca gtg gtg gca ctg      147
275 Thr Gly Ala Leu Glu Val Gln Val Pro Glu Asp Pro Val Val Ala Leu
276                               30                               35                               40
278 gtg ggc acc gat gcc acc ctg tgc tgc tcc ttc tcc cct gag cct ggc      195
279 Val Gly Thr Asp Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly
280                               45                               50                               55
282 ttc agc ctg gca cag ctc aac ctc atc tgg cag ctg aca gat acc aaa      243
283 Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys
284                               60                               65                               70
286 cag ctg gtg cac agc ttt gct gag ggc cag gac cag ggc agc gcc tat      291
287 Gln Leu Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr
288                               75                               80                               85
290 gcc aac cgc acg gcc ctc ttc ccg gac ctg ctg gca cag ggc aac gca      339
291 Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala
292 90                               95                               100                               105
294 tcc ctg agg ctg cag cgc gtg cgt gtg gcg gac gag ggc agc ttc acc      387
295 Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr
296                               110                               115                               120
298 tgc ttc gtg agc atc cgg gat ttc ggc agc gct gcc gtc agc ctg cag      435
299 Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln
300                               125                               130                               135
302 gtg gcc gct ccc tac tcg aag ccc agc atg acc ctg gag ccc aac aag      483
303 Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu Pro Asn Lys
304                               140                               145                               150
306 gac ctg cgg cca ggg gac acg gtg acc atc acg tgc tcc agc tac cag      531
307 Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser Ser Tyr Gln
308                               155                               160                               165
310 ggc tac cct gag gct gag gtg ttc tgg cag gat ggg cag ggt gtg ccc      579
311 Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln Gly Val Pro
312 170                               175                               180                               185
314 ctg act ggc aac gtg acc acg tcg cag atg gcc aac gag cag ggc ttg      627
315 Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu Gln Gly Leu
316                               190                               195                               200
318 ttt gat gtg cac agc atc ctg cgg gtg gtg ctg ggt gca aat ggc acc      675
319 Phe Asp Val His Ser Ile Leu Arg Val Val Leu Gly Ala Asn Gly Thr
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323	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro	Val	Leu	Gln	Gln	Asp	Ala	His	Ser	
324			220					225					230				
326	tct	gtc	acc	atc	aca	ccc	cag	aga	agc	ccc	aca	gga	gcc	gtg	gag	gtc	771
327	Ser	Val	Thr	Ile	Thr	Pro	Gln	Arg	Ser	Pro	Thr	Gly	Ala	Val	Glu	Val	
328			235				240					245					
330	cag	gtc	cct	gag	gac	ccg	gtg	gtg	gcc	cta	gtg	ggc	acc	gat	gcc	acc	819
331	Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp	Ala	Thr	
332	250					255					260					265	
334	ctg	cgc	tgc	tcc	ttc	tcc	ccc	gag	cct	ggc	ttc	agc	ctg	gca	cag	ctc	867
335	Leu	Arg	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	Ala	Gln	Leu	
336				270						275					280		
338	aac	ctc	atc	tgg	cag	ctg	aca	gac	acc	aaa	cag	ctg	gtg	cac	agt	ttc	915
339	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	Val	His	Ser	Phe	
340			285						290					295			
342	acc	gaa	ggc	cgg	gac	cag	ggc	agc	gcc	tat	gcc	aac	cgc	acg	gcc	ctc	963
343	Thr	Glu	Gly	Arg	Asp	Gln	Gly	Ser	Ala	Tyr	Ala	Asn	Arg	Thr	Ala	Leu	
344			300				305						310				
346	ttc	ccg	gac	ctg	ctg	gca	caa	ggc	aat	gca	tcc	ctg	agg	ctg	cag	cgc	1011
347	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala	Ser	Leu	Arg	Leu	Gln	Arg	
348		315					320					325					
350	gtg	cgt	gtg	gcg	gac	gag	ggc	agc	ttc	acc	tgc	ttc	gtg	agc	atc	cgg	1059
351	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	Thr	Cys	Phe	Val	Ser	Ile	Arg	
352	330					335					340				345		
354	gat	ttc	ggc	agc	gct	gcc	gtc	agc	ctg	cag	gtg	gcc	gct	ccc	tac	tcg	1107
355	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser	Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	
356				350					355					360			
358	aag	ccc	agc	atg	acc	ctg	gag	ccc	aac	aag	gac	ctg	cgg	cca	ggg	gac	1155
359	Lys	Pro	Ser	Met	Thr	Leu	Glu	Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	
360			365					370					375				
362	acg	gtg	acc	atc	acg	tgc	tcc	agc	tac	cgg	ggc	tac	cct	gag	gct	gag	1203
363	Thr	Val	Thr	Ile	Thr	Cys	Ser	Ser	Tyr	Arg	Gly	Tyr	Pro	Glu	Ala	Glu	
364			380				385						390				
366	gtg	ttc	tgg	cag	gat	ggg	cag	ggt	gtg	ccc	ctg	act	ggc	aac	gtg	acc	1251
367	Val	Phe	Trp	Gln	Asp	Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	
368		395				400					405						
370	acg	tcg	cag	atg	gcc	aac	gag	cag	ggc	ttg	ttt	gat	gtg	cac	agc	gtc	1299
371	Thr	Ser	Gln	Met	Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	
372	410					415					420					425	
374	ctg	cgg	gtg	gtg	ctg	ggt	gcg	aat	ggc	acc	tac	agc	tgc	ctg	gtg	cgc	1347
375	Leu	Arg	Val	Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	
376				430					435					440			
378	aac	ccc	gtg	ctg	cag	cag	gat	gcg	cac	ggc	tct	gtc	acc	atc	aca	ggg	1395
379	Asn	Pro	Val	Leu	Gln	Gln	Asp	Ala	His	Gly	Ser	Val	Thr	Ile	Thr	Gly	
380			445					450					455				
382	cag	cct	atg	aca	ttc	ccc	cca	gag	gcc	ctg	tgg	gtg	acc	gtg	ggg	ctg	1443
383	Gln	Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu	
384			460					465					470				
386	tct	gtc	tgt	ctc	att	gca	ctg	ctg	gtg	gcc	ctg	gct	ttc	gtg	tgc	tgg	1491

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:1; N Pos. 1309,1310,1311,1312,1313,1314,1315,1316,1317,1318,1319,1320
Seq#:1; N Pos. 1321,1322,1323,1324,1325,1326,1327,1328,1329,1330,1331,1332
Seq#:1; N Pos. 1333,1334,1335,1336,1337,1338,1339,1340,1341,1342,1343,1344
Seq#:1; N Pos. 1345,1346,1347,1348,1349,1350,1351,1352,1353,1354,1355,1356
Seq#:1; N Pos. 1357,1358,1359,1360,1361,1362,1363,1364,1365
Seq#:2; Xaa Pos. 421,422,423,424,425,426,427,428,429,430,431,432,433,434
Seq#:2; Xaa Pos. 435,436,437,438,439,440,441,442,443,444,445,446,447